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SELECTION FOR FIRST PARITY LINEAR-TYPE TRAITS IN THE NEW ZEALAND DAIRY CATTLE POPULATION

M.A. Nilforooshan, R.G. Sherlock and B.L. Harris

Livestock Improvement Corporation, Hamilton 3240, New Zealand

SUMMARY

Unlike production traits, linear-type traits are subjective and expensive to measure. Recording, genetic evaluation and selection for these traits is generally done on the first parity records (2 years of age). It is, however, important to know whether this selection is effective in improving later-in-life performances. This can be assessed by estimating the genetic correlation between early-in-life and later-in-life evaluations of the same trait. Data were extracted from the animals with later-in-life (parities 2–5) phenotypes, and genetic correlations were estimated between the same trait early- and later in life. The estimated genetic correlations of greater than 0.92 indicated that the benefits of early-in-life selection for these traits were retained later in life.

INTRODUCTION

Linear-type traits are among the most economically important traits in the dairy cattle industry. These traits cover and evaluate various aspects of the cow's body conformation, including udder shape and attachment, body frame, and leg structure. Linear-type traits are genetically correlated with production traits (Lin *et al.* 1987), udder health (Rogers *et al.* 1991), lameness (Boettcher *et al.* 1998), and survival (Williams *et al.* 2022). Since these traits are frequently scored in the first parity and genetically correlated with survival in older parities, Williams *et al.* (2022) reported these traits were suitable early predictors of survival for later parity cows. Currently, 15 linear-type traits are routinely evaluated in the New Zealand dairy cattle population (Harris 2022).

It is important to know whether early-in-life (EIL) evaluations are good indicators of later-in-life (LIL) performances for linear-type traits and whether animals selected for EIL performances will perform well LIL. In that case, EIL selection will be effective over an animal's productive life, and the superiority will be passed on to the next generations. This concept can be reformulated to determine whether EIL and LIL observations on the same trait are genetically similar or how strong the genetic × age interaction is for linear-type traits.

In the present study, the effectiveness of EIL (first parity) selection for linear-type traits on the LIL genetic merits was investigated by estimating the genetic correlations between EIL and LIL of the same traits and on the next generation's performance by estimating the heritabilities, in the NZ dairy cattle populations.

MATERIALS AND METHODS

Data. Late (after the first parity or 2 years of age) records on 12 linear type traits were recorded on 7,796 cows, once per cow. Six of these traits were udder conformation traits. Trait names and abbreviations are presented in Table 1. Recording inspections occurred in November-December 2023 and February-March 2024. Contemporary groups were defined as Herd-Inspector-Season. However, since each herd was recorded once and there was no inspector overlap between herds, this definition was equivalent to "Herd". A single record from parity 6 and 67 records from small contemporary groups with less than 5 observations were discarded. All the 7,728 remaining cows in 93 contemporary groups had a single LIL phenotype for all the linear type traits. Table 1 presents the descriptive statistics of the LIL linear type scores. The full definition of the traits can be found in DairyNZ 2020.

Table 1. Trait names and abbreviations, and descriptive statistics of the 7,728 late-in-life (parities 2–5) scores of linear-type traits. The maximum of all the traits is 9

Trait name	Trait abbr.	Min.	Median	Mean	SD
Capacity	CAP	3	7	6.69	0.99
Dairy Conformation	DC	2	7	6.48	1.16
Front Teat Placement	FT	1	5	4.81	0.68
Fore Udder Attachment	FU	1	6	5.65	1.25
Rump Angle	RA	1	4	3.95	0.80
Rear Leg Set	RLS	3	6	6.00	0.61
Rear Teat Placement	RT	2	6	6.49	1.16
Rear Udder Attachment	RU	1	6	5.96	1.12
Rump Width	RW	2	6	5.53	1.08
Stature	ST	2	6	5.75	1.23
Udder Overall Score	UO	1	6	5.80	1.20
Udder Support	US	1	6	6.32	1.14

The definition of EIL contemporary groups (age-'calving season'-herd) differed from that of LIL contemporary groups (herd). For variance components estimation, a pedigree subset including animals with various degrees of relatedness (closely related to unrelated) with the 7,728 animals was extracted from the whole pedigree. Contemporary groups corresponding to EIL records containing any of the 7,728 animals with LIL records, their dams, full-sisters, half-sisters, and progeny were identified. Four generations of parents were extracted from 474,560 animals in those contemporary groups, resulting in a pedigree of 1,369,575 animals and 474,560 EIL animals with phenotype in 7,902 EIL contemporary groups. There were 7,618 animals with phenotypes for both EIL and LIL. Descriptive statistics of the EIL phenotypes are presented in Table 2.

Table 2. Descriptive statistics of the 474,560 early-in-life (parity 1) scores of linear type traits. The minimum and maximum of all the traits are 1 and 9

Trait abbr.*	Median	Mean	SD
CAP	6	6.26	1.03
DC	6	6.31	1.1
FT	5	4.58	0.69
FU	6	5.76	1.12
RA	4	4.44	0.77
RLS	6	6.15	0.63
RT	6	6.16	1.03
RU	6	5.86	1.09
RW	6	5.79	0.98
ST	5	5.50	1.31
UO	6	5.72	1.13
US	6	6.01	1.09

*The full trait names are given in Table 1.

Model. A bivariate model was fitted to EIL (parity 1) and LIL (parities 2–5) of each linear-type trait. Due to the limited number of LIL phenotypes, parities 2 to 5 were combined into a single trait, where a single phenotype was available per phenotyped animal. Since EIL and LIL phenotypes were recorded at different ages, the two were considered residually independent (i.e., residual covariance equal to 0). Both traits (EIL and LIL of each linear-type trait) included random effects of direct additive genetic and residuals. The fixed effects were contemporary groups and covariates for genetic groups, age at calving (AAC), AAC^2, inbreeding coefficient, breed proportions, and heteroses. The EIL model also included Legendre Polynomials of order 4 covariates for days-in-milk. The variance components (genetic covariances and residual variances) were estimated using the AI-REML procedure of the APEX software (GENOMIC COMPUTING PTY LIMITED 2023).

RESULTS AND DISCUSSION

The genetic covariances and residual variances were estimated from the EIL and LIL bivariate analysis of each linear-type trait. Table 3 presents the heritability and genetic correlation estimates from each analysis.

Table 3. The heritability (h^2) and genetic correlation (r_g) estimates between the early-in-life (EIL, parity 1) and later-in-life (LIL, parities 2–5) variates of each linear type trait, in bivariate analyses

Trait abbr.*	h^2_{EIL}	h^2_{LIL}	r_g
CAP	0.270	0.375	0.957
DC	0.204	0.414	0.937
FT	0.267	0.350	0.925
FU	0.245	0.427	0.935
RA	0.331	0.541	0.969
RLS	0.096	0.101	0.995
RT	0.370	0.502	0.969
RU	0.254	0.469	0.935
RW	0.244	0.397	0.929
ST	0.492	0.658	0.974
UO	0.244	0.443	0.935
US	0.257	0.391	0.927

*The full trait names are given in Table 1.

The estimated genetic correlations ranged from 0.925 (FT) to 0.995 (RLS). These high genetic correlations indicate low genetic × age interactions and that EIL linear type traits genetically remain the same trait over time. As such, EIL evaluations are suitable indicators of the corresponding LIL linear-type trait, and cows selected for EIL linear-type traits genetically tend to perform better later in life. Aside from the RLS low heritability, heritabilities were moderate to high, showing great potential for selection on these traits and large gain transferred to the next generation. The LIL heritabilities were higher than those for EIL. The LIL heritabilities are expected to be lower than the EIL heritabilities due to EIL selection. However, higher LIL heritabilities might be due to the low number of LIL records, low selection intensity on the EIL linear type traits, and less important environmental effects in LIL than in EIL for the linear type traits.

There were 2,561, 2,249, 1,705, and 1,213 phenotypes in parity 2 to 5, respectively. With 33.1% of LIL phenotypes belonging to parity 2, there was a risk that the high estimated genetic correlations between EIL and LIL could be due to the short age gap between parity 1 (EIL) and parity 2. In another attempt, the age gap between EIL and LIL was increased by discarding the second parity phenotypes and the variance components estimation analyses were repeated. The results are presented in Table 4. Discarding the second parity, LIL phenotypes caused decreases in the heritabilities of both EIL and LIL traits except for CAP-LIL and RLS-LIL. The estimated genetic correlations between EIL and LIL decreased for most of the traits. Those that did not decrease had a negligible increase. The estimated genetic correlations remained greater than 0.9, indicating that the conclusions made based on the previous results remained valid.

Table 4. The heritability (h^2) and genetic correlation (r_g) estimates between the early-in-life (EIL, parity 1) and later-in-life (LIL, parities 3–5) variates of each linear type trait, in bivariate analyses

Trait abbr.*	h^2_{EIL}	h^2_{LIL}	r_g
CAP	0.267	0.393	0.914
DC	0.199	0.358	0.938
FT	0.264	0.327	0.927
FU	0.241	0.404	0.937
RA	0.324	0.541	0.961
RLS	0.095	0.116	0.977
RT	0.366	0.486	0.966
RU	0.249	0.446	0.935
RW	0.241	0.371	0.945
ST	0.490	0.657	0.975
UO	0.237	0.411	0.902
US	0.253	0.360	0.915

*The full trait names are given in Table 1.

CONCLUSION

Linear-type traits are subjective and expensive to measure. These traits are usually recorded and evaluated in the first parity when the cow is 2 years of age (EIL). Selection is then performed on the EIL evaluations. Whether the selected cows will be genetically superior and perform well later in life is of interest. The high estimated genetic correlations between EIL and LIL of the same linear-type trait confirmed that selection decisions made on EIL evaluations improve LIL performances, and EIL is a good indicator of LIL for linear-type traits. The moderate to high estimated heritabilities showed that selecting these traits will improve the EIL and LIL of the next generation.

REFERENCES

Boettcher P.J., Dekkers J.C., Warnick L.D. and Wells S.J. (1998) *J. Dairy Sci.* **81**: 1148.

DairyNZ (2020) https://www.dairynz.co.nz/media/xsmce10a/top-booklet-2020.pdf (Accessed 10/10/2024).

Genomic Computing Pty Limited (2023) APEX – Linear model suite. https://ghpc.ai/ (Accessed 10/10/2024).

Harris B.L. (2022) *JDS Commun.* **3**: 152.

Lin C.Y., Lee A.J., McAllister A.J., Batra T.R., Roy G.L., Veseley A.J., Wauthy J.M. and Winter K.A. (1987) *J. Dairy Sci.* **70**: 2385.

Rogers G.W., Hargrove G.L., Lawlor T.J. and Ebersole J.L. (1991) *J. Dairy Sci.* **74**: 1087.

Williams M., Sleator R.D., Murphy C.P., McCarthy J. and Berry D.P. (2022) *J. Dairy Sci.* **105**: 7550.